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RAW SEQUENCE LISTING

DATE: 09/10/2001

PATENT APPLICATION: US/08/855,402A

TIME: 08:10:33

Input Set : A:\Bradfiel.app

Output Set: N:\CRF3\09102001\H855402A.raw

3 <110> APPLICANT: Bradfield, Christopher A.
 4 Dolwick, Kristin M.
 5 Carver, Lucy A.
 7 <120> TITLE OF INVENTION: Ah Receptor cDNAs and Genetically Engineered Cells for
 8 Detecting Agonists to the Ah Receptor
 10 <130> FILE REFERENCE: HYBRIDZYME
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/08/855,402A
 C--> 13 <141> CURRENT FILING DATE: 1997-05-13
 15 <160> NUMBER OF SEQ ID NOS: 40
 17 <170> SOFTWARE: PatentIn Ver. 2.1
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 3207
 21 <212> TYPE: DNA
 22 <213> ORGANISM: murine
 24 <220> FEATURE:
 25 <221> NAME/KEY: CDS
 26 <222> LOCATION: (1)..(2415)
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 30 Met Ser Ser Gly Ala Asn Ile Thr Tyr Ala Ser Arg Lys Arg Arg Lys
 31 1 5 10 15
 33 ccg gtg cag aaa aca gta aag ccc atc ccc gct gaa gga att aag tca 96
 34 Pro Val Gln Lys Thr Val Lys Pro Ile Pro Ala Glu Gly Ile Lys Ser
 35 20 25 30
 37 aat cct tct aag cga cac aga gac cgg ctg aac aca gag tta gac cgc 144
 38 Asn Pro Ser Lys Arg His Arg Asp Arg Leu Asn Thr Glu Leu Asp Arg
 39 35 40 45
 41 ctg gcc agc ctg ctg ccc ttc ccg caa gat gtt att aat aag ctg gac 192
 42 Leu Ala Ser Leu Leu Pro Phe Pro Gln Asp Val Ile Asn Lys Leu Asp
 43 50 55 60
 45 aaa ctc tct gtt ctt agg ctc agc gtc acg tac ctg agg gcc aag agc 240
 46 Lys Leu Ser Val Leu Arg Leu Ser Val Thr Tyr Leu Arg Ala Lys Ser
 47 65 70 75 80
 49 ttc ttt gat gtt gca tta aag tcc acc cct gct gac aga aat gga ggc 288
 50 Phe Phe Asp Val Ala Leu Lys Ser Thr Pro Ala Asp Arg Asn Gly Gly
 51 85 90 95
 53 cag gac cag tgt aga gca caa atc aga gac tgg cag gat ttg caa gaa 336
 54 Gln Asp Gln Cys Arg Ala Gln Ile Arg Asp Trp Gln Asp Leu Gln Glu
 55 100 105 110
 57 gga gag ttc ttg tta cag gcg ctg aat ggc ttt gtg ctg gtt gtc aca 384
 58 Gly Glu Phe Leu Leu Gln Ala Leu Asn Gly Phe Val Leu Val Val Thr
 59 115 120 125
 61 gca gat gcc ttg gtc ttc tat gct tcc tcc act atc caa gat tac ctg 432
 62 Ala Asp Ala Leu Val Phe Tyr Ala Ser Ser Thr Ile Gln Asp Tyr Leu
 63 130 135 140
 65 ggc ttt cag cag tct gat gtc atc cat cag agc gta tat gag ctc atc 480
 66 Gly Phe Gln Gln Ser Asp Val Ile His Gln Ser Val Tyr Glu Leu Ile

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67 145          150          155          160
69 cat aca gaa gac cgg gcg gaa ttc cag cgc cag ctt cac tgg gct cta 528
70 His Thr Glu Asp Arg Ala Glu Phe Gln Arg Gln Leu His Trp Ala Leu
71          165          170          175
73 aac cca gac tct gca caa gga gtg gac gaa gcc cat ggc cct cca cag 576
74 Asn Pro Asp Ser Ala Gln Gly Val Asp Glu Ala His Gly Pro Pro Gln
75          180          185          190
77 gca gca gtc tat tat acc cca gac cag ctt cct cca gag aac gct tct 624
78 Ala Ala Val Tyr Tyr Thr Pro Asp Gln Leu Pro Pro Glu Asn Ala Ser
79          195          200          205
81 ttc atg gag agg tgc ttc agg tgc cgg ctg agg tgc ctg ctg gat aat 672
82 Phe Met Glu Arg Cys Phe Arg Cys Arg Leu Arg Cys Leu Leu Asp Asn
83          210          215          220
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86 Ser Ser Gly Phe Leu Ala Met Asn Phe Gln Gly Arg Leu Lys Tyr Leu
87 225          230          235          240
89 cat gga cag aac aag aaa ggg aag gac gga gcg ctg ctt cct cca caa 768
90 His Gly Gln Asn Lys Lys Gly Lys Asp Gly Ala Leu Leu Pro Pro Gln
91          245          250          255
93 ctg gct ttg ttt gca ata gct act cca ctt cag cca ccc tcc atc ctg 816
94 Leu Ala Leu Phe Ala Ile Ala Thr Pro Leu Gln Pro Pro Ser Ile Leu
95          260          265          270
97 gaa att cga acc aaa aac ttc atc ttc agg acc aaa cac aag cta gac 864
98 Glu Ile Arg Thr Lys Asn Phe Ile Phe Arg Thr Lys His Lys Leu Asp
99          275          280          285
101 ttc aca cct att ggt tgt gat gcc aaa ggg cag ctt att ctg ggc tat 912
102 Phe Thr Pro Ile Gly Cys Asp Ala Lys Gly Gln Leu Ile Leu Gly Tyr
103          290          295          300
105 aca gaa gta gag ctg tgc aca aga gga tcg ggg tac cag ttc atc cat 960
106 Thr Glu Val Glu Leu Cys Thr Arg Gly Ser Gly Tyr Gln Phe Ile His
107 305          310          315          320
109 gct gca gac ata ctt cac tgt gca gaa tcc cac atc cgc atg att aag 1008
110 Ala Ala Asp Ile Leu His Cys Ala Glu Ser His Ile Arg Met Ile Lys
111          325          330          335
113 act gga gaa agt ggc atg aca gtt ttc cgg ctt ctt gca aaa cac agt 1056
114 Thr Gly Glu Ser Gly Met Thr Val Phe Arg Leu Leu Ala Lys His Ser
115          340          345          350
117 cgc tgg agg tgg gtc cag tcc aat gca cgc ttg att tac aga aat gga 1104
118 Arg Trp Arg Trp Val Gln Ser Asn Ala Arg Leu Ile Tyr Arg Asn Gly
119          355          360          365
121 aga cca gat tac atc atc gcc act cag aga cca ctg acg gat gaa gaa 1152
122 Arg Pro Asp Tyr Ile Ile Ala Thr Gln Arg Pro Leu Thr Asp Glu Glu
123          370          375          380
125 gga cga gag cat tta cag aag cga agt acg tcg ctg ccc ttc atg ttt 1200
126 Gly Arg Glu His Leu Gln Lys Arg Ser Thr Ser Leu Pro Phe Met Phe
127 385          390          395          400
129 gct acc gga gag gct gtg ttg tac gag atc tcc agc cct ttc tct ccc 1248
130 Ala Thr Gly Glu Ala Val Leu Tyr Glu Ile Ser Ser Pro Phe Ser Pro
131          405          410          415

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133	ata atg gat ccc cta cca ata cgc acc aaa agc aac act agc agg aaa	1296
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137	gac tgg gct ccc cag tca acc cca agt aag gat tct ttc cac ccc agt	1344
138	Asp Trp Ala Pro Gln Ser Thr Pro Ser Lys Asp Ser Phe His Pro Ser	
139	435 440 445	
141	tct ctt atg agt gcc ctg atc cag cag gat gag tcc atc tat ctg tgt	1392
142	Ser Leu Met Ser Ala Leu Ile Gln Gln Asp Glu Ser Ile Tyr Leu Cys	
143	450 455 460	
145	cct cct tca agc cct gcg ctg tta gac agc cat ttt ctg atg ggc tcc	1440
146	Pro Pro Ser Ser Pro Ala Leu Leu Asp Ser His Phe Leu Met Gly Ser	
147	465 470 475 480	
149	gtg agc aag tgc ggg agt tgg caa gac agc ttt gcg gcc gca gga agt	1488
150	Val Ser Lys Cys Gly Ser Trp Gln Asp Ser Phe Ala Ala Ala Gly Ser	
151	485 490 495	
153	gag gct gcg ctg aaa cat gag caa att ggc cat gct cag gac gtg aac	1536
154	Glu Ala Ala Leu Lys His Glu Gln Ile Gly His Ala Gln Asp Val Asn	
155	500 505 510	
157	ctt gca ctg tct ggc ggc ccc tca gag ctg ttt ccg gat aat aaa aat	1584
158	Leu Ala Leu Ser Gly Gly Pro Ser Glu Leu Phe Pro Asp Asn Lys Asn	
159	515 520 525	
161	aat gac ttg tac agc atc atg agg aac ctt ggg att gat ttt gaa gat	1632
162	Asn Asp Leu Tyr Ser Ile Met Arg Asn Leu Gly Ile Asp Phe Glu Asp	
163	530 535 540	
165	atc aga agc atg cag aac gag gag ttc ttc aga act gac tcc acc gct	1680
166	Ile Arg Ser Met Gln Asn Glu Glu Phe Phe Arg Thr Asp Ser Thr Ala	
167	545 550 555 560	
169	gct ggt gag gtt gac ttc aaa gac atc gac ata acg gac gaa atc ctg	1728
170	Ala Gly Glu Val Asp Phe Lys Asp Ile Asp Ile Thr Asp Glu Ile Leu	
171	565 570 575	
173	acc tac gtg cag gat tcc ctg aac aat tca act ttg ctg aac tcg gct	1776
174	Thr Tyr Val Gln Asp Ser Leu Asn Asn Ser Thr Leu Leu Asn Ser Ala	
175	580 585 590	
177	tgc cag cag cag cct gtg act cag cac cta agc tgt atg ctg cag gag	1824
178	Cys Gln Gln Gln Pro Val Thr Gln His Leu Ser Cys Met Leu Gln Glu	
179	595 600 605	
181	cgc ctg caa cta gag caa cag caa cag ctt cag cag ccc ccg ccg cag	1872
182	Arg Leu Gln Leu Glu Gln Gln Gln Gln Leu Gln Gln Pro Pro Pro Gln	
183	610 615 620	
185	gct ctg gag ccc cag cag cag ctg tgt cag atg gtg tgc ccc cag caa	1920
186	Ala Leu Glu Pro Gln Gln Gln Leu Cys Gln Met Val Cys Pro Gln Gln	
187	625 630 635 640	
189	gat ctg ggt ccg aag cac acg caa atc aac ggc acg ttt gca agt tgg	1968
190	Asp Leu Gly Pro Lys His Thr Gln Ile Asn Gly Thr Phe Ala Ser Trp	
191	645 650 655	
193	aac ccc acc cct ccc gtg tct ttc aac tgt ccc cag cag gaa cta aag	2016
194	Asn Pro Thr Pro Pro Val Ser Phe Asn Cys Pro Gln Gln Glu Leu Lys	
195	660 665 670	
197	cac tat cag ctg ttt tcc agc tta cag ggg act gct cag gaa ttt ccc	2064

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199          675          680          685
201 tac aaa cca gag gtg gac agt gtg cct tac aca cag aac ttt gct ccc 2112
202 Tyr Lys Pro Glu Val Asp Ser Val Pro Tyr Thr Gln Asn Phe Ala Pro
203          690          695          700
205 tgt aat cag cct ctg ctt cca gaa cat tcc aag agt gtg cag ttg gac 2160
206 Cys Asn Gln Pro Leu Leu Pro Glu His Ser Lys Ser Val Gln Leu Asp
207 705          710          715          720
209 ttc cct gga agg gat ttt gaa ccg tcc ctg cat ccc act act tct aat 2208
210 Phe Pro Gly Arg Asp Phe Glu Pro Ser Leu His Pro Thr Thr Ser Asn
211          725          730          735
213 tta gat ttt gtc agt tgt tta caa gtt cct gaa aac caa agt cat ggg 2256
214 Leu Asp Phe Val Ser Cys Leu Gln Val Pro Glu Asn Gln Ser His Gly
215          740          745          750
217 ata aac tca cag tcc gcc atg gtc agt cct cag gca tac tat gct ggg 2304
218 Ile Asn Ser Ser Gln Ser Ala Met Val Ser Pro Gln Ala Tyr Tyr Ala Gly
219          755          760          765
221 gcc atg tcc atg tat cag tgc cag cca ggg cca cag cgc acc cct gtg 2352
222 Ala Met Ser Met Tyr Gln Cys Gln Pro Gly Pro Gln Arg Thr Pro Val
223          770          775          780
225 gac cag acg cag tac agc tct gaa att cca ggt tct cag gca ttc cta 2400
226 Asp Gln Thr Gln Tyr Ser Ser Glu Ile Pro Gly Ser Gln Ala Phe Leu
227 785          790          795          800
229 agc aag gtg cag agt tgagggtgttt tcaatgaaac ctattcgtcc gacttgagca 2455
230 Ser Lys Val Gln Ser
231          805
233 gcattggcca cgctgctcag accactggcc atctccatca ctgcggaagc ccggcctctt 2515
235 ccgatataca caccgggtgg attcctgtag ctcccatgcc aggatgaaat tcattcagga 2575
237 acaggatacc agaactgtga ggggttgaca tcagtacact ttctccaaaa cagatttcga 2635
239 ttcttggtgt tagagaagga gtttaaaacc cgtacctgag atgctcccta tacgatggga 2695
241 gagctcggac ggagcacatg ggaggagttc aggcacctca gaggtcacag tgtttactgt 2755
243 gaaaaattct cgggttccct gctcagtaac ttcagcagga aaaacaggga ggtatttgga 2815
245 gctttgaact tctggattct tgtagtata ccaaatacgg agttacagga ctaaccgatt 2875
247 tctatatatt ttaacctct gttttgtcc cagaagttaa agtaaattgg ttggtgcttt 2935
249 tctcaaaaga aaatctcaat gctttcttcc tgcactgtta atataagtgc ctcacttttt 2995
251 gttgtgtgtg ttgtgtgttt ctgatttttt tcttttttcc tatctacctg taacacaata 3055
253 ggggtatgtat ttatatatgaa atatttttta tcttttttga attaatattc tttctgcaca 3115
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262 <212> TYPE: PRT
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272 Asn Pro Ser Lys Arg His Arg Asp Arg Leu Asn Thr Glu Leu Asp Arg

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273          35          40          45
275 Leu Ala Ser Leu Leu Pro Phe Pro Gln Asp Val Ile Asn Lys Leu Asp
276          50          55          60
278 Lys Leu Ser Val Leu Arg Leu Ser Val Thr Tyr Leu Arg Ala Lys Ser
279 65          70          75          80
281 Phe Phe Asp Val Ala Leu Lys Ser Thr Pro Ala Asp Arg Asn Gly Gly
282          85          90          95
284 Gln Asp Gln Cys Arg Ala Gln Ile Arg Asp Trp Gln Asp Leu Gln Glu
285          100          105          110
287 Gly Glu Phe Leu Leu Gln Ala Leu Asn Gly Phe Val Leu Val Val Thr
288          115          120          125
290 Ala Asp Ala Leu Val Phe Tyr Ala Ser Ser Thr Ile Gln Asp Tyr Leu
291          130          135          140
293 Gly Phe Gln Gln Ser Asp Val Ile His Gln Ser Val Tyr Glu Leu Ile
294 145          150          155          160
296 His Thr Glu Asp Arg Ala Glu Phe Gln Arg Gln Leu His Trp Ala Leu
297          165          170          175
299 Asn Pro Asp Ser Ala Gln Gly Val Asp Glu Ala His Gly Pro Pro Gln
300          180          185          190
302 Ala Ala Val Tyr Tyr Thr Pro Asp Gln Leu Pro Pro Glu Asn Ala Ser
303          195          200          205
305 Phe Met Glu Arg Cys Phe Arg Cys Arg Leu Arg Cys Leu Leu Asp Asn
306          210          215          220
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309 225          230          235          240
311 His Gly Gln Asn Lys Lys Gly Lys Asp Gly Ala Leu Leu Pro Pro Gln
312          245          250          255
314 Leu Ala Leu Phe Ala Ile Ala Thr Pro Leu Gln Pro Pro Ser Ile Leu
315          260          265          270
317 Glu Ile Arg Thr Lys Asn Phe Ile Phe Arg Thr Lys His Lys Leu Asp
318          275          280          285
320 Phe Thr Pro Ile Gly Cys Asp Ala Lys Gly Gln Leu Ile Leu Gly Tyr
321          290          295          300
323 Thr Glu Val Glu Leu Cys Thr Arg Gly Ser Gly Tyr Gln Phe Ile His
324 305          310          315          320
326 Ala Ala Asp Ile Leu His Cys Ala Glu Ser His Ile Arg Met Ile Lys
327          325          330          335
329 Thr Gly Glu Ser Gly Met Thr Val Phe Arg Leu Leu Ala Lys His Ser
330          340          345          350
332 Arg Trp Arg Trp Val Gln Ser Asn Ala Arg Leu Ile Tyr Arg Asn Gly
333          355          360          365
335 Arg Pro Asp Tyr Ile Ile Ala Thr Gln Arg Pro Leu Thr Asp Glu Glu
336          370          375          380
338 Gly Arg Glu His Leu Gln Lys Arg Ser Thr Ser Leu Pro Phe Met Phe
339 385          390          395          400
341 Ala Thr Gly Glu Ala Val Leu Tyr Glu Ile Ser Ser Pro Phe Ser Pro
342          405          410          415
344 Ile Met Asp Pro Leu Pro Ile Arg Thr Lys Ser Asn Thr Ser Arg Lys
345          420          425          430

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Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY

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L:12 M:270 C: Current Application Number differs, Replaced Application Number

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:909 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5

L:930 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6